

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1441.15 Seconds
(without alignments)
15778.007 Million cell updates/sec

Title: US-09-497-967-5

Perfect score: 1404

Sequence: 1 atgaagaacaacactctggt.....tgatctcttactactgctg 1404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	54.4	3.9	502	14	BQ134889
C 2	54.4	3.9	590	14	BQ135179
C 3	54.4	3.9	602	14	BQ135164
C 4	54.4	3.9	607	14	BQ134912
C 5	54.4	3.9	658	14	BQ135057
C 6	51.2	3.6	445	14	BQ134871

C 7	50.4	3.6	419	14	BQ135036
C 8	40	2.8	210	14	BQ134900
C 9	40	2.8	538	14	BQ134810
C 10	40	2.8	592	14	BQ134985
C 11	40	2.8	599	14	BQ134821
C 12	40	2.8	661	14	BQ135189
C 13	40	2.8	675	14	BQ135196
C 14	40	2.8	856	9	AL529709
C 15	39.8	2.8	565	12	BF191747
C 16	39.4	2.8	946	17	CNS06Q63
C 17	38.6	2.7	938	13	BI950738
C 18	37.8	2.7	390	13	BI316601
C 19	37.8	2.7	1089	17	CNS06Q06
C 20	37.8	2.7	1089	17	CNS06P2J
C 21	37.6	2.7	479	12	BF776376
C 22	37.4	2.7	413	12	BG156079
C 23	37.4	2.7	977	17	CNS02ANA
C 24	37.2	2.6	941	17	CNS056AV
C 25	37	2.6	1177	13	EG915930
C 26	36.8	2.6	877	17	CNS04NWK
C 27	36.6	2.6	328	10	BB497602
C 28	36.4	2.6	576	9	AL818926
C 29	36.2	2.6	389	10	AW325085
C 30	36.2	2.6	448	12	BF255972
C 31	36.2	2.6	473	13	BM098087
C 32	36.2	2.6	576	12	BG301223
C 33	36.2	2.6	688	9	AI612588
C 34	36.2	2.6	791	9	AJ443260
C 35	36.2	2.6	894	12	BG367203
C 36	35.8	2.5	256	12	BG301587
C 37	35.8	2.5	273	13	BM339376
C 38	35.8	2.5	424	9	AI438101
C 39	35.8	2.5	447	12	BF707190
C 40	35.8	2.5	513	10	BE355071
C 41	35.8	2.5	654	13	BI874624
C 42	35.8	2.5	669	9	AU169066
C 43	35.8	2.5	713	17	AZ346186
C 44	35.8	2.5	862	12	BG769770
C 45	35.8	2.5	920	12	BG420157

ALIGNMENTS

RESULT 1
BQ134889/c
LOCUS
DEFINITION
BQ134889
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ134889
INIT1_1_D07.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis CDNA, mRNA sequence.
502 bp mRNA linear EST 22-APR-2002
multifiliis CDNA, mRNA sequence.
BQ134889.1 GI:20260988
EST.
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 502)
Clark, I., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 474

BQ135036 INIT1_2_D
BQ134900 INIT1_1_E
BQ134810 INIT1_4_C
BQ134985 INIT1_2_G
BQ134821 INIT1_4_D
BQ135189 INIT1_4_D
BQ135196 INIT1_4_E
AL529709 AL529709
BF191747 239419 MA
AL410257 T7 end of
BI950738 HVSME1002
BI316601 saf05d09.
AL411124 T7 end of
AL410021 T3 end of
BF776376 287167 MA
BG156079 sea80a12.
AL188711 Tetraodon
AL323104 Tetraodon
BG915930 602815385
AL299261 Tetraodon
BB497602 BB497602
AL818926 AL818926
AW325085 TENUA4390
BF255972 HVSME1000
BM098087 BBP103_SO
BG301223 HVSMEB001
AI612588 TENG0393
AJ443260 AJ443260
BG367203 HVSME1001
BG301587 kt02h09.y
BM339376 MEST240-F
AI438101 sa35h11.y
BF707190 282711 MA
BE355071 DGI_113.G
BI874624 963116H11
AU169066 AU169066
AZ346186 LM0881G06
BG769770 602744673
BG420157 602452258

/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into Lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 215 a 122 c 122 g 199 t
ORIGIN

Query Match 3.98; Score 54.4; DB 14; Length 658;
Best Local Similarity 51.78; Pred. No. 0.00084;
Matches 155; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

QY 1114 GCTACCTGATCGCTCAGTGTCTGCTGAGTGTCTGCTGGAACCGTGTGACCGACGGA 1173
DB 315 GCTACTTCAGCCACATATATGTAAACGATGTCCTGCTGCTGCTGCTGATGATGGT 256
QY 1174 ACCACCTTACCTACACAGCGCTGCTTCTGAGTGTGTGAAGTGTGCTTAACCTTCTAC 1233
DB 255 ACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTACTTAATGTTAGGCTAACTTTTAT 196
QY 1234 ACCACCAACGACGAGCTGGTGGCTGGAATCGACACCTGTACCTCTGTGTAAACAAG 1293
DB 195 GCATCAAAACATCTGGTTTGCACAGGTACTGATACATGCTGATGTTCTTAAAAA 136
QY 1294 CTGACCTCTGGAGCTGAGGCTAACCTGCTGAGTGTGCTTAAGAAGACATCCAGTGTGAC 1353
DB 135 TTAACCTTCTGGTGTACAGCTAAAGTATATCTGGAAGCTACTTAAAGACATAATGCGCC 76
QY 1354 -----TTGCGTAACCTCTGCTATCTCTGCTGCTGCTGCTGCTTCTTACTACCTGCTG 1404
DB 75 AGTTCACCTTTCGCAAAATTTTATCAATGCTTAAATATTATTCTTCTTCTTATTTGTTG 16

RESULT 6
BQ134871/c
LOCUS
DEFINITION
INIT1_B05.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

ACCESSION BQ134871
VERSION BQ134871.1 GI:20260970
KEYWORDS EST
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
REFERENCE 1 (bases 1 to 445)
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
TITLE Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
JOURNAL An EST database for Ichthyophthirius multifiliis (G5 isolate)
COMMENT Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence start: 37
High quality sequence stop: 443
POLYA=Yes.
FEATURES
source Location/Qualifiers
1..445
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into Lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 155 a 79 c 71 g 140 t
ORIGIN

Query Match 3.68; Score 51.2; DB 14; Length 445;
Best Local Similarity 51.08; Pred. No. 0.005;
Matches 153; Conservative 0; Mismatches 138; Indels 9; Gaps 1;

QY 1114 GCTACCTGATCGCTCAGTGTCTGCTGAGTGTCTGCTGGAACCGTGTGACCGACGGA 1173
DB 323 GCTACTTCAGCCACATATATGTAAACGATGTCCTGCTGCTGCTGATGATGGT 264
QY 1174 ACCACCTTACCTACACAGCGCTGCTTCTGAGTGTGTGAAGTGTGCTTAACCTTCTAC 1233
DB 263 TCATCAACTAATTTTGTAGCTTTAGCAAGTGAATGCTCTAAATGTTAGGCTAACTTTTAT 204
QY 1234 ACCACCAACGACGAGCTGGTGGCTGGAATCGACACCTGTACCTCTTGTAAACAAG 1293
DB 203 GCATCAAAACATCTGGTTTGCACAGGTACTGATACATGCTGATGTTCTTAAAAA 144
QY 1294 CTGACCTCTGGAGCTGAGGCTAACCTGCTGAGTGTGCTTAAGAAGACATCCAGTGTGAC 1353
DB 143 TTAACCTTCTGGTGTACAGCTAAAGTATATCTGGAAGCTACTTAAAGACATAATGCGCC 84
QY 1354 -----TTGCGTAACCTCTGCTATCTCTGCTGCTGCTGCTTCTTACTACCTGCTG 1404
DB 83 AGTTCACCTTTCGCAAAATTTTATCAATGCTTAAATATTATTCTTCTTCTTATTTGCGC 24

RESULT 7
BQ135036/c
LOCUS
DEFINITION
INIT1_D10.gl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

ACCESSION BQ135036
VERSION BQ135036.1 GI:20261135
KEYWORDS EST
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
REFERENCE 1 (bases 1 to 419)
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
TITLE Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
JOURNAL An EST database for Ichthyophthirius multifiliis (G5 isolate)
COMMENT Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 306
High quality sequence stop: 419
POLYA=Yes.
FEATURES
source Location/Qualifiers
1..419
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"

KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 599)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
COMMENT Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 593 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 506
POLYA-No..

FEATURES Location/Qualifiers
source 1..599
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 191 a 113 c 111 g 183 t 1 others
ORIGIN

Query Match 2.8%; Score 40; DB 14; Length 599;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1114 GCTACCGTGATGCGTCAGTGTGCTCTGAGTGTCTCTGCAACGGTCTCACCGACGGA 1173
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 349 GCTAAATTAGCGCAATAATGGCACTGAATGTCTCTGCGCACTCTTGTGTACAGACGGA 290
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1174 ACCACCTTCACTACAAGCAGGCTCTCTGAGTGTGTGAAGTGTGCTGCTAACTTCTAC 1233
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 289 GTAAACCTTACTATATCTGATCATCTCTCAATGTGTTAATGTTAAAGTGCGCTTTTAC 230

RESULT 12
LOCUS BQ135189 661 bp mRNA linear EST 22-APR-2002
DEFINITION INIT1.4_D09_g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION BQ135189
VERSION BQ135189.1 GI:20261288
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 661)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
COMMENT Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Search completed: February 16, 2003, 22:25:06
Job time : 1454.15 secs

[illegible]